

## SEQUENCE LISTING

<110> ENEA-Ente per le Nuove Tecnologie e l'Ambiente  
Consiglio Nazionale delle Ricerche

<120> Method for the preparation of transgenic plants characterised by  
Geminivirus lasting resistance

<130> PCT25622

<140> RM2003A000242  
<141> 2003-05-19

<150> RM2003A000242  
<151> 2003-05-19

<160> 12

<170> PatentIn version 3.2

<210> 1  
<211> 630  
<212> DNA  
<213> Geminivirus TYLCSV

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ccaaccaggt cagcacattt ccatccgaac attcaggag ctaaatacgag ctccgacgtc 300  
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cattttcata atataaatag taatttagat aaggttttcc aggtgcctcc ggcaccttat 540  
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<223> TYLCSV Rep-210 modified sequence

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Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg  
 35 40 45  
 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe  
 50 55 60  
 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80  
 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu  
 100 105 110  
 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
 115 120 125  
 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser  
 130 135 140  
 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu  
 145 150 155 160  
 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro  
 165 170 175  
 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val  
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 1 5 10 15

48

aca tac ccc aag tgt gac tta act aag gag aat gca ttg tcc cag ata 96  
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 Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg  
 35 40 45  
 gaa ctt cac gag aat gga gaa cca cat ctt cat atc ttg ata cag ttc 192  
 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe  
 50 55 60  
 gaa ggc aag tat aac tgc acc aac caa cgt ttc ttt gac ctt gtg tcc 240  
 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80  
 cct acc aga tca gcc cat ttt cat cca aac atc cag ggt gct aag tcg 288  
 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
 agt tca gac gtg aag tca tac att gac aaa gac ggg gat gtg ctc gag 336  
 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu  
 100 105 110  
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 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
 115 120 125  
 aca gca aac gat gca tac gct aag gct atc aac gct gga tcc aag tca 432  
 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser  
 130 135 140  
 cag gca ctt gac gta atc aaa gag tta gct cct agg gat tat gtt ctt 480  
 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu  
 145 150 155 160  
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 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro  
 165 170 175  
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 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val  
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 cca gat gag ctt gag cat tgg gtg tct gaa aac gtt atg gac gcc gca 624  
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 Pagina 4

20

25

30

Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg  
 35 40 45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe  
 50 55 60

Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu  
 100 105 110

Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
 115 120 125

Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser  
 130 135 140

Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu  
 145 150 155 160

His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro  
 165 170 175

Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val  
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 195 200 205

Ala Arg  
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gtg cgt agg aga ctt aac ttt gac tct ccg tac acc tct cgt gca gct Val Arg Arg Arg Leu Asn Phe Asp Ser Pro Tyr Thr Ser Arg Ala Ala	96
gct ccc aca gtc cag ggc att aag agg cga tct tgg aca tac aga cct Ala Pro Thr Val Gln Gly Ile Lys Arg Arg Ser Trp Thr Tyr Arg Pro	144
atg tac agg aaa ccg agg atg tat agg atg tat cgt agc cca gat gtg Met Tyr Arg Lys Pro Arg Met Tyr Arg Met Tyr Arg Ser Pro Asp Val	192
cct cct ggt tgc gaa gga ccc tgc aag gtg caa tcg tat gag caa cgt Pro Pro Gly Cys Glu Gly Pro Cys Lys Val Gln Ser Tyr Glu Gln Arg	240
gac gat gtg aag cac acc gga gtt gtt cgt tgc gtt tct gat gtg act Asp Asp Val Lys His Thr Gly Val Val Arg Cys Val Ser Asp Val Thr	288
aga ggt tca ggt atc act cac agg gtg gga aag cgt ttc tgt att aag Arg Gly Ser Gly Ile Thr His Arg Val Gly Lys Arg Phe Cys Ile Lys	336
tct att tac ata ttg ggt aag atc tgg atg gac gag aat atc aag aaa Ser Ile Tyr Ile Leu Gly Lys Ile Trp Met Asp Glu Asn Ile Lys Lys	384
cag aat cac act aat cag gtt atg ttc ttt ctt gtg cga gat cga aga Gln Asn His Thr Asn Gln Val Met Phe Phe Leu Val Arg Asp Arg Arg	432
cca tac gga acc agc cca atg gac ttc ggc cag gtg ttt aat atg ttc Pro Tyr Gly Thr Ser Pro Met Asp Phe Gly Gln Val Phe Asn Met Phe	480
gat aac gag cca tct act gca act gtg aaa aat gat ttg cgt gat aga Asp Asn Glu Pro Ser Thr Ala Thr Val Lys Asn Asp Leu Arg Asp Arg	528
tat cag gtg atg aga aag ttc cat gca acg gtg gtt ggt ggt cct tct Tyr Gln Val Met Arg Lys Phe His Ala Thr Val Val Gly Gly Pro Ser	576
gga atg aaa gag caa tgt ctt ctg aaa aga ttc ttt aag atc aac act Gly Met Lys Glu Gln Cys Leu Leu Lys Arg Phe Phe Lys Ile Asn Thr	624
cat gtc gtc tat aac cac cag gag caa gcg aaa tat gag aat cac act His Val Val Tyr Asn His Gln Glu Gln Ala Lys Tyr Glu Asn His Thr	672
gaa aat gct ttg ttg tta tac atg gcc tgt acc cac gca tct aat cca Glu Asn Ala Leu Leu Leu Tyr Met Ala Cys Thr His Ala Ser Asn Pro	720
gtt tac gca acg ctt aag atc cgt atc tat ttc tat gac gct gtg aca Val Tyr Ala Thr Leu Lys Ile Arg Ile Tyr Phe Tyr Asp Ala Val Thr	768
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<220>  
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 35 40 45

Met Tyr Arg Lys Pro Arg Met Tyr Arg Met Tyr Arg Ser Pro Asp Val  
 50 55 60

Pro Pro Gly Cys Glu Gly Pro Cys Lys Val Gln Ser Tyr Glu Gln Arg  
 65 70 75 80

Asp Asp Val Lys His Thr Gly Val Val Arg Cys Val Ser Asp Val Thr  
 85 90 95

Arg Gly Ser Gly Ile Thr His Arg Val Gly Lys Arg Phe Cys Ile Lys  
 100 105 110

Ser Ile Tyr Ile Leu Gly Lys Ile Trp Met Asp Glu Asn Ile Lys Lys  
 115 120 125

Gln Asn His Thr Asn Gln Val Met Phe Phe Leu Val Arg Asp Arg Arg  
 130 135 140

Pro Tyr Gly Thr Ser Pro Met Asp Phe Gly Gln Val Phe Asn Met Phe  
 145 150 155 160

Asp Asn Glu Pro Ser Thr Ala Thr Val Lys Asn Asp Leu Arg Asp Arg  
 165 170 175

Tyr Gln Val Met Arg Lys Phe His Ala Thr Val Val Gly Gly Pro Ser  
 180 185 190

Gly Met Lys Glu Gln Cys Leu Leu Lys Arg Phe Phe Lys Ile Asn Thr  
 195 200 205

His Val Val Tyr Asn His Gln Glu Gln Ala Lys Tyr Glu Asn His Thr  
 210 215 220

Glu Asn Ala Leu Leu Leu Tyr Met Ala Cys Thr His Ala Ser Asn Pro  
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 <222> (51)..(443)

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 <222> (231)..(231)  
 <223> Point mutation from C (Rep-210 wild-type) to T

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 <222> (233)..(233)  
 <223> Point mutation from C (Rep 210 wild-type) to G

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 Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe Leu Thr Tyr  
 5 10 15  
 ccc aaa tgt gat tta aca aaa gaa aat gca ctt tcc caa ata aca aac 152  
 Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile Thr Asn  
 20 25 30  
 cta caa aca ccc aca aac aaa tta ttc atc aaa att tgc aga gaa cta 200  
 Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg Glu Leu  
 35 40 45 50  
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 His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe Glu Gly  
 55 60 65  
 aaa tac aat tgt acc aat caa cga ttc ttc gac ctg gta tcc cca acc 296  
 Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser Pro Thr  
 70 75 80  
 agg tca gca cat ttc cat ccg aac att cag gga gct aaa tcg agc tcc 344  
 Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser  
 85 90 95  
 gac gtc aag tcc tat atc gac aag gac gga gat gtt ctt gaa tgg ggt 392  
 Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu Trp Gly  
 100 105 110  
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447

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Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg  
 35 40 45

Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe  
 50 55 60

Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu  
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Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
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Thr Ala  
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 <222> (1)..(30)  
 <223> Primer for PCR C4 mutagenesis

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<210> 12  
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 <212> DNA  
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 gaaaatcata ctgagaatgc cttgttattg tatatggctt gtactcatgc ttctaaccga 720  
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